

## Appendix II

Alignment of instant SEQ ID NO: 1 (nucleotides 770-1310) with SEQ ID NO: 27  
(plasmid pMG) of Perkins et al

>ic1|61939 SID\_27  
Length=5627

Sort alignments for this  
E value Score Percent  
Query start position

Score = 765 bits (414), Expect = 0.0  
Identities = 414/414 (100%), Gaps = 0/414 (0%)  
Strand=Plus/Plus

Query	770	GCCAAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCACCCGCTTGGCTTCTTAT	829
Subject	1879	GCCAAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCACCCGCTTGGCTTCTTAT	1938
Query	830	GCATGCTATACCTGTTTTTGGCTTGGGCTCTATACACCCCGCTTCTCATGTTATAGGTG	889
Subject	1939	GCATGCTATACCTGTTTTTGGCTTGGGCTCTATACACCCCGCTTCTCATGTTATAGGTG	1998
Query	890	ATGGTATAGCTTAGCCTATAGGTGTTGGTTATTGACCATTTATGACCACTCCCTATTGG	949
Subject	1999	ATGGTATAGCTTAGCCTATAGGTGTTGGTTATTGACCATTTATGACCACTCCCTATTGG	2058
Query	950	TGACGATACCTTTCCATTACTAATCCATAACATGGGCTCTTGCCACAACCTCTTTATTGG	1009
Subject	2059	TGACGATACCTTTCCATTACTAATCCATAACATGGGCTCTTGCCACAACCTCTTTATTGG	2118
Query	1010	CTATATGCCAATACACTGTCTCTCAGAGACTGACACGGACTCTGTATTTTACAGGATGG	1069
Subject	2119	CTATATGCCAATACACTGTCTCTCAGAGACTGACACGGACTCTGTATTTTACAGGATGG	2178
Query	1070	GGTCTCATTTTATTTTACAAATTCACATATACAACACCCGCTCCCGAGTSCCCGCGAGT	1129
Subject	2179	GGTCTCATTTTATTTTACAAATTCACATATACAACACCCGCTCCCGAGTSCCCGCGAGT	2238
Query	1130	TTTTATTAAACATAACGTGGGATCTCCACGCGAATCTCGGGTACGTGTTCCGGA	1183
Subject	2239	TTTTATTAAACATAACGTGGGATCTCCACGCGAATCTCGGGTACGTGTTCCGGA	2292

Score = 215 bits (116), Expect = 4e-59  
Identities = 116/116 (100%), Gaps = 0/116 (0%)  
Strand=Plus/Plus

Query	1183	AACGGTGGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTGCGCGCGCGCCACCAAGACA	1242
Subject	2607	AACGGTGGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTGCGCGCGCGCCACCAAGACA	2666
Query	1243	TAATAGCTGACAGACTAACAGACTGTTCCTTTTCCATGGGCTTTTCTGCACTCACC	1298
Subject	2667	TAATAGCTGACAGACTAACAGACTGTTCCTTTTCCATGGGCTTTTCTGCACTCACC	2722